Listing of Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

1 – 35. **(Cancelled)**

36. **(New)** A method of designing a drug capable of affecting LTA_4 hydrolase protein activity utilizing a molecular structure of an LTA_4 hydrolase protein or a part, functionally equivalent part, derivative or conformational analogue thereof, wherein the molecular structure is defined by the coordinates defining atom 1 to atom 4876 as set forth in Table 9.

37. **(New)** The method of claim 36, wherein the method involves a technique selected from the group consisting of molecular modeling, direct structure based design, and combinatorial chemistry.

38. **(New)** The method of claim 36, wherein the LTA_4 hydrolase protein comprises an enzymatically active site as defined by the following table:

	Left Wall	Right Wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

39. **(New)** The method of claim 36, wherein the LTA_4 hydrolase protein comprises an enzymatically active site defined by the following amino acids Gln136; Ala137; Tyr267;

Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

40. **(New)** The method of claim 36, wherein the LTA_4 hydrolase protein comprises an enzymatically active site defined by the following amino acids Gln136; Ala 137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val367; Leu369; Pro374; Asp375; lle372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

41. **(New)** The method of claim 36, wherein the drug is an agonist or inhibitor of LTA_4 hydrolase protein activity.

42. **(New)** The method of claim 41, further comprising the steps of

a) employing a conventional organic synthesis, alone or in combination with combinatorial chemistry; and

b) refining the structure of the product of the synthesis by cycles of crystallisation of the LTA_4 hydrolase and either the inhibitor or agonist,

wherein steps a and b are performed at least once.

43. **(New)** The method of claim 36, wherein the drug is for the treatment or prevention of at least one disorder selected from the group consisting of acute inflammatory symptoms, chronic inflammatory symptoms, acute allergic symptoms and chronic allergic symptoms.

44. **(New)** The method of claim 36, wherein the drug is for the treatment or prevention of a disorder selected from the group consisting of arthritis, inflammatory bowel disease (IBD), psoriasis, chronic obstructive pulmonary disease (COPD) and acquired immune deficiency syndrome (AIDS).

45. **(New)** The method of claim 36, wherein the drug is for the treatment or prevention of a proliferative disorder.

46. **(New)** The method of claim 45, wherein the proliferative disorder is a neoplasia or cancer.

47. **(New)** The method of claim 36, wherein the drug is for the treatment or prevention of a disorder caused by *Bacillus anthracis*.

48. **(New)** The method of claim 47, wherein the disorder is anthrax.

49. **(New)** A method of identifying a compound capable of interacting with a LTA_4 hydrolase protein, comprising utilizing a molecular structure of an LTA_4 hydrolase protein or a part, functionally equivalent part, derivative or conformational analogue thereof, in a preliminary screening method, wherein the molecular structure is defined by the coordinates defining atom 1 to atom 4876 as set forth in Table 9.

50. **(New)** The method of claim 49, wherein the LTA_4 hydrolase protein comprises an enzymatically active site as defined by the following table:

	Left Wall	Right Wall
1		Lys608, Asp606, Lys605, Lys354, Thr355
2	Phe356, Phe362	Gln544, Asp573, Lys572, Arg568
3	Val376	Lys565, Arg540, Leu507
4	Ser380, Ser352, Glu348	Pro569
5	Tyr378, Glu348	Arg563, Glu533, Phe536, Arg537, Tyr267
6	Tyr383, Phe314, Glu318, Glu384, Arg326	
7	Gly268, Gly269, Met270	His295, Asn341, Phe340
8	Ser288, His497	Glu325, Asn291

51. **(New)** The method of claim 49, wherein the LTA_4 hydrolase protein comprises an enzymatically active site defined by the following amino acids Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; Lys565.

52. **(New)** The method of claim 49, wherein the LTA_4 hydrolase protein comprises an enzymatically active site defined by the following amino acids Gln136; Ala 137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val367; Leu369; Pro374; Asp375; lle372; Ala377; Pro382; Tyr378; Tyr383; Arg563; Lys565.

53. **(New)** The method of claim 49, wherein the compound is an agonist or inhibitor of LTA_4 hydrolase protein activity.

54. **(New)** The method of claim 49, further comprising the steps of comparing the molecular structure, or a selected region thereof, with the three dimensional structure of the compound using computer modeling techniques.

55. **(New)** The method of claim 49, wherein the compound is complementary to a region of the LTA_4 hydrolase.

56. **(New)** The method of claim 55, wherein the compound is complementary to an enzymatically active site of the LTA_4 hydrolase.

57. **(New)** The method of claim 49, wherein the compound is a general metallohydrolase inhibitor.

58. **(New)** The method of claim 49, wherein the compound inhibits epoxide hydrolase activity or aminopeptidase activity of LTA_4 hydrolase or LTA_4 syntheses.

59. **(New)** The method of claim 49, wherein the compound antagonizes LTB_4 receptor binding of a cell.